

OM of: US-09-805-550-2 to: EST: * out_format : pfs

Date: Aug 31, 2002 4:58 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+ .p2n.model -DEV=xih
-O=/cgn2_1/USPO.spool/US0980550/cunat_29082002.160721_29030/app-query.fasta.1.897
-DB=EST -OPMT=fastap -SUPFL=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPT=0.000 -LOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELDP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blotsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=0.000 -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEADSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US0980550.6CGN1.1.3201
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NCPY -WAIT -THREADS=1

Search information block:

Query: US-09-805-550-2
Query length: 405

Database: EST: *

Database sequences: 13736207

Database length: -1841457050

Search time (sec): 2392.770000

Sequence	Strid	Orig	ZScore	EScore	len	Document
gb_est1:AM331091	+	1012.00	1185.19	9.1e-57	657	AM331091 707047803.xl 707 - MIX
gb_est1:AM155658	+	955.00	1119.64	4.1e-53	589	AM155658 614097011.yl 614 - ROC
gb_est1:AM057042	+	937.00	1098.77	5.9e-52	580	AM057042 66000808.xl 660 - MIX
gb_est1:AT881646	+	925.00	1083.29	4.3e-51	685	AT881646 606071012.yl 606 - EST
gb_est1:BE602523	+	895.00	1047.66	1.1e-49	735	BE602523 HVSMH0099114f Hordeum
gb_est1:AT151316	+	884.00	1037.00	1.6e-48	575	AT151316 IPL_70.A12.bl.A002 Imm
gb_est1:BF586471	+	870.50	1020.91	1.3e-47	597	BF586471 ESM_28.E12.bl.A003 FIC
gb_est1:BI925179	+	837.00	979.67	2.5e-45	761	BI925179 ESM_28.E12.bl.A003 FIC
gb_est1:BG445098	+	817.50	955.27	5.7e-44	899	BG445098 GA_Ea0026608f Gossyp
gb_est1:AM399956	+	812.00	952.43	8.5e-44	623	AM399956 707053508.xl 707 - MIX
gb_est1:BM078237	+	808.00	946.76	1.7e-43	685	BM078237 MEST116-H10.T3 ISDM4-T
gb_est1:AM000280	+	803.00	942.63	2.9e-43	565	AM000280 614010804.yl 614 - roc
gb_est1:BG445328	+	781.50	914.35	1.1e-41	810	BG445328 GA_Ea0027122f Gossyp
gb_est1:BG365760	+	781.50	913.36	1.3e-41	906	BG365760 HVSMH0004B16f Hordeum
gb_est1:AV928200	+	774.00	906.28	3.1e-41	750	AV928200 AV928200 K. Sato unpu
gb_est1:BF586390	+	753.00	894.82	1.4e-40	642	BF586390 FMI_28.E12.g1.A003 FIC
gb_est1:AM508593	+	759.50	890.11	2.5e-40	689	AM508593 614097011.yl 614 - MIX
gb_est1:BG585286	+	757.00	885.68	4.4e-40	817	BG585286 EST487049 MHAM Medicag
gb_est1:BI305515	+	756.50	888.47	3.1e-40	559	BI305515 NL_0.E13 Drought stres
gb_est1:BM337351	+	753.00	882.39	6.7e-40	700	BM337351 MEST149-E08.T3 ISDM5-R
gb_est1:AM331092	+	751.00	880.24	8.8e-40	685	AM331092 707047803.yl 707 - MIX
gb_est1:BE035647	+	746.50	871.93	2.5e-39	967	BE035647 MO13A05 MO Mesembryant
gb_est1:BG415925	+	739.00	865.54	5.8e-39	741	BG415925 HVSMH0009B06f Hordeum
gb_est1:AM092601	+	734.50	860.62	1.1e-38	714	AM092601 AU097027 Rice shoot O
gb_est1:AV097027	+	734.50	859.45	1.1e-38	714	AV097027 AU097027 Rice callus C
gb_est1:BG458891	+	725.00	848.52	5.1e-38	801	BG458891 EST490800 MHRP-Medicag
gb_est1:BE704885	+	721.50	844.26	8.9e-38	817	BE704885 SC01_02C08.A SC01 AACD
gb_est1:BF292870	+	721.00	846.90	6.3e-38	568	BF292870 WHE2165.H04.P0725 Triti
gb_est1:BM380735	+	716.00	839.60	1.6e-37	670	BM380735 MEST524-C09.univ ISDM6
gb_est1:BG048096	+	715.50	839.03	1.7e-37	669	BG048096 sae07906.yl Gm-cl058 G
gb_est1:AI947481	+	715.00	841.08	1.3e-37	487	AI947481 614047804.xl 614 - roc
gb_est1:BG445485	+	711.50	831.93	4.3e-37	890	BG445485 GA_Ea0028806f Gossyp
gb_est1:BE357293	+	707.50	830.55	5.1e-37	607	BE357293 DGL_148.C01.bl.A002 Da
gb_est1:BE357080	+	702.50	826.51	8.6e-37	496	BE357080 DGL_24.C07.bl.A002 Dat
gb_est1:BM113219	+	695.50	815.40	3.6e-36	691	BM113219 EST560755 potato roots
gb_est1:BM266651	+	695.00	815.18	3.7e-36	663	BM266651 MEST384-H08.T3 ISDM5-R
gb_est1:BE357362	+	692.00	813.62	4.5e-36	533	BE357362 DGL_148.C01.g1.A002 Da
gb_est1:AV922620	+	690.00	809.75	7.4e-36	634	AV922620 AV922620 K. Sato unpu
gb_est1:BE214515	+	687.00	805.14	1.3e-35	718	BE214515 HV_Ceb0003K2f Hordeum
gb_est1:BE917857	+	686.50	806.23	1.2e-35	595	BE917857 OVL_7.A02.bl.A002 Ovar

gb_est2:BF272420 + 686.50 803.33 1.7e-35 825 | BF272420 GA_Ea001AN15f Goss
gb_est2:BG344194 + 686.00 802.81 1.8e-35 819 | BG344194 HVSMH0008A20f Hord
gb_est2:BI211965 + 682.50 801.77 2.1e-35 581 | BI211965 IPL_62.F12.bl.A002
gb_est2:BF067283 + 681.50 799.94 2.6e-35 626 | BF067283 st37908.yl Gm-cl067
gb_est1:AV932070 + 681.50 799.65 2.7e-35 647 | AV932070 AV932070 K. Sato un

seq_name: gb_est1:AM331091

seq_documentation_block:

LOCUS AM331091 657 bp mRNA linear EST 31-JAN-2000
DEFINITION 707047803.xl 707 - Mixed adult tissues from Walbot lab (SK) Zea
ACCESSION AM331091.1 GI:6827448
VERSION AM331091.1
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 657)
Walbot, V.
University
Maize ESTs from various cDNA libraries sequenced at Stanford

REFERENCE

AUTHORS Walbot, V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL

COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 725 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707047 row: B column: 03.
Location/Qualifiers
1. 657
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10b"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
vector: pGAD10; Site: 1; EcorI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Undirectionally cloned."

FEATURES

source

BASE COUNT 158 a 182 c 161 g 156 t
ORIGIN
alignment_scores:
Quality: 1012.00 Length: 218
Ratio: 4.842 Gaps: 0
Percent Similarity: 95.872 Percent Identity: 92.202
alignment_block:
US-09-805-550-2 x AM331091 ..
Align seg 1/1 to: AM331091 from: 1 to: 657

119 AAlaThrAlaGlnTrpAlaProSerValGlnProGlnAlaAlaProAl 135
|||||
3 GCCACAGCTGAAGCGACCTCCAGTCACAGACTCGCTGCCAGC 52
GCCACAGCTGAAGCGACCTCCAGTCACAGACTCGCTGCCAGC 52
135 aAlaThyValAlaAlaTrpAspAlaAspValIySerGlnAlaAla 152
|||||
53 TGCACAGCTGCTGATCGATGATGATGATGATGATGATGATGATG 102
TGCACAGCTGCTGATCGATGATGATGATGATGATGATGATGATG 102
152 eAsnIleValIaPhgIaAsnAsnLeuGluGlnTrpIleGlnIleLeu 168
|||||
103 CGAACCTTGATCAAGGACCAACTGACAGACTATTCAACAAATTC 152
CGAACCTTGATCAAGGACCAACTGACAGACTATTCAACAAATTC 152


```

seq_name: gb_est1:AW057042
seq_documentation_block:
LOCUS      AW057042                580 bp    mRNA    linear    EST 29-SEP-1999
DEFINITION 660008A08.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,
            mRNA sequence.
ACCESSION   AW057042
VERSION     AW057042.1  GI:5932681
KEYWORDS    EST.
SOURCE      Zea mays.
            Zea mays.
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            Clade; Panicoidae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 580)
AUTHORS     Walbot,V.
TITLE       Maize ESTs from various cDNA libraries sequenced at Stanford
            University
JOURNAL     Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 660008 row: A column: 08.
            Location/Qualifiers
                source          1..580
                /organism="Zea mays"
                /cultivar="Ohio43"
                /db_xref="taxon:4577"
                /clone_lib="660 - Mixed stages of anther and pollen"
                /tissue_type="Whole premeiotic anthers to pollen shed"
                /dev_stage="premeiotic anthers to pollen shed"
                /lab_host="XJOLR"
                /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                Site_2: XhoI; Anther and pollen cDNA library.
                Directionally sequenced with 5' end at the EcoRI site.
                Created by Amie Franklin."
BASE COUNT  136 a      160 c      139 g      145 t
ORIGIN
118 ValAlaThrAlaGluThrAlaProSerValGlnProGlnAlaAlaPr 134
14 GTTGCACACAGCTGAACGGCAGCTCCAGTCCAGCTCAGCTGCC 63
134 GaaAlaAlaThrValAlaAlaThrAspAlaAspValAlaSerGlnAla 151
64 AGCTGCTACGGTGTGCTGCTACTGATGCTGATGCTGATGCTGATGCTG 113
151 laSerAsnLeuValPheGlyAsnAsnLeuGlnGlnThrIleGlnGlnIle 167
114 CTTCACAACTTGTATCTGGCAACAATCTAGACACTATCCAAACAATT 163
168 LeuAspMetGlyGlyGlyThrTTPGluArgAspThrValValArgAlaLe 184
164 CTTCAGATGCTGTGTGTATCATGGAACCTGATACCTGTTGCTGCTCT 213
184 uATGAlaAlaATyrAsnAsnProGluArgAlaIleAspTyrLeuTyrSerG 201
214 ACCTGCTGCATACATTAACCCCGAGAGAGCTATAGCTACTGATTTCTG 263

```

```

201 lylleProGluAsnValGluAlaGlnProValAlaArgAlaProAlaAla 217
264 GAATTCCTGAGAAATGTGAGAGCTCAGCTGTGCTGCCGAGCAGCTGCTG 313
218 GlyGlnGlnThrAsnGlnGlnAlaAlaSerProAlaGlnProAlaValAl 234
314 GGCCAAACAAACAAATCAGCAGCGGCATCCGCTCCAGCAGCAGTTCG 363
234 aleProValGlnProSerProAlaSerAlaGlyProAsnAlaAsnProL 251
364 ATTCGCCAGTGCAGCCATCACCCTGCTGTGCAGGCGCCCTTAATGCAATCTT 413
251 euAsnLeuPheProGlnGlyValProSerGlyGlySerAsnProGlyVal 267
414 TGAACCTTTTCCACAGGCTTCACAGTGTGGGTGCACACCCAGTGTG 463
268 ValProGlyAlaGlySerGlyAlaAlaLeuAspAlaLeuArgGlnLeuProG 284
464 GTTCAGAGTGCAGAGATCTGTGCTCTTGATGCTTGCGACAGCTTCACA 513
284 nPheGlnAlaLeuGlnLeuValGlnAlaAsnProGlnIleLeuGlnP 301
514 GTTCAAGCACTCCTTCATGTTAGTCCAGGCTAATCCTCAATCTTGACAC 563
301 roketleuGln 304
564 CAATGCTTAG 574
seq_name: gb_est1:AI881646
seq_documentation_block:
LOCUS      AI881646                685 bp    mRNA    linear    EST 02-FEB-2000
DEFINITION 606071D12.y1 606 - Ear tissue cDNA library from Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   AI881646
VERSION     AI881646.1  GI:5566780
KEYWORDS    EST.
SOURCE      Zea mays.
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            Clade; Panicoidae; Andropogoneae; Zea.
            1 (bases 1 to 685)
REFERENCE   1
AUTHORS     Walbot,V.
TITLE       Maize ESTs from various cDNA libraries sequenced at Stanford
            University
JOURNAL     Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 606071 row: D column: 12.
            Location/Qualifiers
                source          1..685
                /organism="Zea mays"
                /cultivar="Ohio43"
                /db_xref="taxon:4577"
                /clone_lib="606 - Ear tissue cDNA library from Schmidt
                lab"
                /tissue_type="mixed"
                /dev_stage="ear length from 0.5 cm - 2.0 cm"
                /note="Organ: Immature ear; Vector: pBK-CMV; Site_1: EcoRI
                ; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
                lab"
BASE COUNT  184 a      187 c      174 g      140 t
ORIGIN

```

alignment_scores:

Quality: 925.00 Length: 191
 Ratio: 4.894 Gaps: 0
 Percent Similarity: 98.953 Percent Identity: 98.953

alignment_block:

US-09-805-550-2 x AT881646 ..

Align seg 1/1 to: AT881646 from: 1 to: 685

```

1 MetLysLeuAsnValLysThrLeuYsglyThrAsnPhgLIuIleGluAl 17
110 ATGAGCGTTAAAGCTCAAGACCTCAAGGCGACCACTTGACATGAGAGC 159
17 AserProAspAlaSerValAlaAspValLysArgIleIleGlyThrThg 34
150 GAGCCCCCAATGCATCGTTGCTGATGTGAGAGATCATATTGACACACTC 209
34 InGIgIAserThrTyrrArgAlaAspGlnGlnMetLeuIleTyrgIngly 50
210 AAGGTCAGAGTACTACCGGGCGGACGACCAATGCTCATATACCAAGGG 259
51 LysIleLeuLysAspGluThrThrLeuGluSerAsnGlyValAlaGluAs 67
260 AAAATTCTCAAGAGTGAACCACTTTGGAAACCAAGGAGTTGCTGAGAGA 309
67 nSerPheLeuValIleMetLeuSerLysAlaLysAlaSerSerSergIya 84
310 CAGCTTCCCTGTTATATGTTGTCCAGGCTTAAGGCATCATGAGTGGAG 359
84 laSerThrAlaThrThrAlaLysAlaProAlaThrLeuAlaGlnProAla 100
360 CTTTCAACGCTACTACTGCAAAAGCTCTGCAACTGTGGCCCAACCTGCT 409
101 AlaProValAlaProAlaAlaSerValAlaArgThrProThrGlnAlaPr 117
410 GCCCGTGGGCCCTGCTGCTGATGAGTGGCAAGACACACAGAGCTCC 459
117 oValAlaThrAlaGluThrAlaProProSerValGlnProGlnAlaAlaPr 134
460 TGTGTCCACAGCTGAACGGCCACTCCAAAGTGTCCAACTCGAGCTGCTC 509
134 roAlaAlaThrValAlaAlaThrAspAlaAspAlaThrSerGlnAla 150
510 CAGCTGCTACAGGTTCTCTGCTACTGATGATGCTGATGCTACAGTCA 559
151 AlaSerAsnLeuValPheGlyAsnAsnLeuGlnGlnThrIleGlnGlnI 167
560 GCTTCAAACTGTATCTGGCAACAATCTAGAACAGACTATCCACAAT 609
167 eLeuAspMetGlyGlyGlyThrTTPGluArgAspThrValAlaArgAlaL 184
610 TCTTACACATGGTGTGCTGATGAGAGCTGATGCTGTTGCTGCTC 659
184 euArgAlaAlaTyrrAsnAsnPro 191
660 TACGTGCTGACATACATAACCG 682

```

seq_name: gb_est2:BE602523

seq_documentation_block:

LOCUS BE602523 735 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSMEH009J14f Hordeum vulgare 5-45 DAP spike EST library

HYCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH009J14f,
 mRNA sequence.

ACCESSION BE602523

VERSION BE602523 GI:13190364

KEYWORDS

SOURCE

ORGANISM Hordeum vulgare

barley.
 Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 735)
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu,
 Y., Henry, D., Palmer, M., Rambo, T., Simmons, D., Choi, D.W., Fenton,
 R.D., Close, S.J., Oates, R. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex 5-45 DAP spike cDNA library
 Unpublished (2001)
 On Aug 21, 2000 this sequence version replaced gi:9860084.
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Total hg bases = 500
 Seq primer: AATTAACCTCCTCAAGG
 High quality sequence start: 12
 High quality sequence stop: 609.
 Location/Qualifiers

FEATURES

source

```

1..735
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH009J14f"
/clone_id="Hordeum vulgare 5-45 DAP spike EST library"
/hycdna0009 (5 to 45 DAP)
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SD Close, Yu Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pluescript SK(-) cDNA phageids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phageids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gppages/bgn/31/cover.html)"

```

BASE COUNT 179 a 186 c 199 g 171 t

ORIGIN

alignment_scores:

Quality: 895.00 Length: 219
 Ratio: 4.520 Gaps: 2
 Percent Similarity: 90.411 Percent Identity: 82.648

alignment_block:

US-09-805-550-2 x BE602523 ..

Align seg 1/1 to: BE602523 from: 1 to: 735

```

188 TyrrAsnAsnProGluArgAlaIleAspTyrrLeuYrSergIyIleProG 204
|||||
10 TATACCAACCCCTGAGAGGGCTATTGACTACGTTCTGGAATATCGTGA 59
204 uAsnValGluAlaGlnProValAlaArgAlaProAlaIleGlyGlnGlnT 221

```

```

60 ATCCGAGAGAGCCCACTGTGTGCTGAGCACTGCTCTGCTCAACAGG 109
221 hr...AnsgInGlnAlaAAserProAlaGlnProAlaValAlaLeuPro 236
110 CAAAGAACCGCAGAGGCTCATCTCAGGCTCAGGCTGCACTACCGGCA 159
237 ValGlnProSer...ProAlaSerAlaGlyProAsnAlaAsnProLeuAs 252
160 GTGCACCACTGCTGTGTGCTCTGCTGCGCCCTAAATCCGAATCCTCTAAA 209
252 nleuPheProGlnGlyValProSerGlyGlySerAsnProGlyValValP 269
210 CCTTTCCCAAGAGGTGTCCAAAGTGGGGCCAAATGCTGTGTGTGTG 259
269 roGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnLeuProGlnPhe 285
260 TGGGTGCGCGGTGCGGCTGATGATGATGATGATGATGATGATGATG 309
286 GlnAlaLeuLeuGlnLeuValGlnAlaAsnProGlnLeuGlnProme 302
310 CAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359
302 tleuGlnGlnLeuGlyGlyGlnAsnProGlnLeuArgLeuGlnGln 319
360 GCTTCAAGAGCTGGGGAACAAATCCACAGATCTGCGGTGATTCAGG 409
319 luanGlnAlaGlnPheLeuArgLeuValAsnGlnSerProGlnGlyGly 335
410 AAATCAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 459
336 ProGlyGlyAsnLeuGlnGlnLeuAlaAlaValProGlnThrLe 352
460 GCTGCGGGAATATCTAGGCGCAGCTCAATGCCACAGGCGAT 509
352 uThrValThrProGlnGlnArgGlnAlaGlnArgLeuGlnGlyMetG 369
510 TCAAGTACTCCAGAAAGACGGAAGCCATCCAGCGGCTTGAGCAATGG 559
369 lypPheAsnArgGlnLeuValLeuGlnValPhePheAlaCysAsnLysP 385
560 GGTTCATGCTGAGCTGTGTGTGAGGCTCTTTCATGATCAACAGGAT 609
386 GlnGlnLeuThrAlaAsnTyrLeuLeuAspHisGlyHisGlnPheAsp 402
610 GAAGAAGCTGCTGCAACTATCTTTGGATCATGCGCAGAGTTGAGGA 659
402 pGlnGln 404
660 ACAACAA 666
seq_name: gb_est2:B1351316
seq_documentation_block:
LOCUS B1351316 575 bp mRNA linear EST 31-UTL-2001
DEFINITION lpl_70_A12.b1_A002 Immature pannicle 1 (lpl) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION B1351316
VERSION B1351316.1 GI:15045758
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 575)
AUTHORS Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and Pratt
,L.H.
TITLE An EST database from Sorghum: developing preanthesis pannicles
JOURNAL Unpublished (2001)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia

```

```

Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmp@pratt.uga.edu
Sequences have been trimmed to exclude polyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three prime sequences, which are obtained with PolYTrix or T7
sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 457
POLYA-No.

FEATURES
    source          location/qualifiers
    1..575          /organism="Sorghum bicolor"
                    /db_xref="taxon:4558"
                    /clone_lib="Immature pannicle 1 (lpl)"
                    /note="Organ: Developing preanthesis pannicles; Vector:
                    Bluescript IT SK(-) from lambda Zap II; Site_1: XhoI;
                    Site_2: EcoRI; The library was made from poly-A RNA in the
                    cloning vector lambda Zap II. Clones to be sequenced were
                    prepared by mass excision."
BASE COUNT      137 a      147 c      155 g      136 t
ORIGIN
alignment_scores:
    Quality: 884.00      Length: 182
    Ratio: 4.966      Gaps: 0
    Percent Similarity: 97.802      Percent Identity: 94.505
alignment_block:
US-09-805-550-2 x B1351316 ..
Align seg 1/1 to: B1351316 from: 1 to: 575
224 GlnAlaAlaSerProAlaGlnProAlaValAlaLeuProValGlnProse 240
6 AGGCGCTCCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 55
240 rProAlaSerAlaGlyProAsnAlaAsnProLeuAsnLeuPheProGln 257
56 CGGTGCTCTGCGAGGCGCTATGCAAAATCCTCTAACCTTTTCTCAGG 105
257 lylValProSerGlyGlySerAsnProGlyValValProGlyAlaGlySer 273
106 GTTCCCAAGTGGTGGGGCCATTCAGGTGTGTTCACAGGTGCGAGATCT 155
274 GlyAlaLeuAspAlaLeuArgGlnLeuProGlnPheGlnAlaLeuGln 290
156 GGTGCCCTTGATGCTTGGCGACAGCTTCCACAGTTTCAAGCACATGCTCA 205
290 nleuValGlnAlaAsnProGlnLeuGlnProMetLeuGlnGlnLeuG 307
206 GTTGTGTCAGGCTAATCTTCAATCTTACAGCCCAATGCTTCAAGATAG 255
307 lylYsgInAsnProGlnLeuArgLeuGlnGlnGlnGlnGlnGlnGln 323
256 GCAAGCAAAACCCCAAAATCTGCGGTGATTCAGGAATAATCAAGCTGAG 305
324 PheLeuArgLeuValAsnGlnSerProGlnGlyGlyProGlyGlyAsn 340
306 TTCTCCCGCTTGGTGAATGAATCCCTGAGAGGTGTGCTGAGGAAACAT 355
340 eleuGlyGlnLeuAlaAlaValProGlnThrLeuThrValThrProG 357
356 ACTAGGTCACTGAGCTGATGCTCAAAAGCTGACGGTTACACAG 405
357 lueGlnArgGlnAlaGlnArgLeuGlnGlyMetGlyPheAsnArgGln 373
406 AGGAACGGAGGCAATCCAGCGCTTGAGGGGAGATGGGTTCAACCGTAG 455
374 leuValLeuGlnValPhePheAlaCysAsnLysAspGlnLeuThrAl 390

```

```

|||||
456 CATGCGCATGAAGTTTCTTTCATGACAAAGGAGAGACTTGGCC 505
390 aasntyrleuLeuaspHisGlyHisGluPheaspArgInglIn 405
|||||
506 CAACCTACCTCTGATCATGGCCATGATTTGACGAGCAGCA 551
seq_name: gb_est2:BF586471

seq_documentation_block:
LOCUS BF586471 597 bp mRNA linear EST 12-DEC-2000
DEFINITION FM1.28_E12.D1.A003 Floral-Induced Meristem 1 (FM1) Sorghum
PROPINGUUM cDNA, mRNA sequence.
ACCESSION BF586471
VERSION BF586471.1 GI:11678795
KEYWORDS EST.
SOURCE Sorghum propinquum.
ORGANISM Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Sorghum.
1 (bases 1 to 597)
Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and Pratt
/L.H.
REFERENCE An EST database from Sorghum: floral-induced meristems
AUTHORS Unpublished (2000)
JOURNAL Contact: Cordonnier-Pratt MM
COMMENT Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: empratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 534
POLYA-NO.

FEATURES
Source
1..597
/organism="Sorghum propinquum"
/db_xref="taxon:132711"
/clone.lib="Floral-Induced Meristem 1 (FM1)"
/note="Organ: Floral-Induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda Zap II. Clones to be sequenced were prepared by
mass excision."

BASE COUNT 154 a 161 c 151 g 131 t
ORIGIN

alignment_scores:
Quality: 870.50 Length: 194
Ratio: 4.655 Gaps: 1
Percent Similarity: 96.392 Percent Identity: 92.784

alignment_block:
US-09-805-550-2 x BF586471 ..
Align seg 1/1 to: BF586471 from: 1 to: 597
1 MetLysLeuAsnValLysThrLeuysGlyThraSpnGluIleGluAl 17
|||||
14 ATGAAGCTTAACGTCAGACCCCTCAAGGCGACCAACTTCGAGATCGAGGC 63
17 aSerProAspAlaSerValAlaAspValLysArgIleIleGluThrTrnG 34

```

```

|||||
64 GAGCCCGGATGCGTGCTGCTGAGGTGAAGAGATCATGAGACCCTC 113
34 lnglyGlnSerThrTyrArgAlaAspGlnGlnMetLeuIleTyrGlnly 50
|||||
114 AGGCTCAGAGTACCTACCAACCGGACAGACCAATATCTCATACCAAGG 163
51 LysIleLeuLysAspGluThrThrLeuGlnSerAsnGlyValAlaGluAs 67
164 AAAATCTTCAGAGATGAGACCACTTGGAAAGCAACGAGGTGCTGAGAA 213
67 nSerPheLeuValIleMetLeuSerLysAlaLysAlaSerSerGlyA 84
214 CAGCTTCCTGTTATATATGTTCTCCAGGCTAAGGCATCGTCACTGAG 263
84 lAserThrAlaThrThrAlaLysAlaProAlaThrLeuAlaGlnProAla 100
|||||
264 CTTTACTGCTACTGCTGCAAAAGCTCCGCAACCTCCGCCCAACTGCT 313
101 .....AlaProValAlaProAlaAlaSerValAlaAlaTyrProTh 114
314 GCACCTGTAGCCCTGTGGCCCTGCTCATCATGTTGCAAGAACACTAC 363
114 rGlnAlaProValAlaThrAlaGluThrAlaProProSerValGlnProG 131
364 ACAAGCTCCTGTTGCCACAGCTGAAACGACACCTCCAGTGACAGCCCTC 413
131 lAlaAlaProAlaAlaThrValAlaAlaThrAspAspAlaAspAlaTyr 147
414 AGCGTCTCTCTGCTCTACGATCGTTCGATCGTGGATGATGCTATGTCAC 463
148 SerGlnAlaAlaSerAsnLeuValPheGlyAsnAsnLeuGlnThrTl 164
464 AGTCAGGAGAGCTTCAACCTGTATCTGGCAACAATCTAGAACACACTAT 513
164 eGlnGlnIleLeuAspMetGlyGlyGlyThrTrpGluThrArgAspThrVal 181
514 CCACCAAAATTTCTTGACATGGGTGGTGTCTTGAGAGCTGATACAGTTG 563
181 aAlaArgAlaLeuArGAlaAlaAlaTyrAsnAspPro 191
564 TCCGTCCTCTACGTCGCTCATATATAACCT 595
seq_name: gb_est2:BI925179

seq_documentation_block:
LOCUS BI925179 761 bp mRNA linear EST 18-OCT-2001
DEFINITION EST545068 tomato flower, buds 0-3 mm Lycopersicon esculentum cDNA
clone CP0A25B24 5' end, mRNA sequence.
ACCESSION BI925179
VERSION BI925179.1 GI:16230294
KEYWORDS EST.
SOURCE Lycopersicon
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanales; Solanales; Solanum;
Lycopersicon.
1 (bases 1 to 761)
van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,
Uterback,T., Van Aken,S., Romning,C.M., Nierman,M., Fraser,C.M.,
Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato flower tissue, 0-3 mm buds (2001)
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers

```

```

source
1. 761
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CTOA25B24"
/clone_lib="tomato flower, buds 0-3 mm"
/tissue_type="flower"
/dev_stage="0-3mm buds"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

BASE COUNT      181 a      197 c      196 g      187 t
ORIGIN

alignment_scores:
Quality:      837.00      Length:      264
Ratio:        3.753      Gaps:      5
Percent Similarity: 84.470      Percent Identity: 66.667

alignment_block:
US-09-805-550-2 x B1925179 ..

Align seg 1/1 to: B1925179 from: 1 to: 761

130 ProGlnAlaAlaProAlaAlaThrValAlaAlaThrAspAlaAspVal 146
|||||
8 CCGGCTCTGCTCTGCTATCGCTGTGTCTG.....GGATCTAGTGT 51
|||||
146 IYrSerGlnAlaAlaSerAsnLeuValPheGlnAsnLeuGlnT 163
|||||
52 CTAATGCGCAAGCTGCTCAAGCTGTGTGCTGTAACAACCTGATGGAG 101
|||||
163 hIleGlnGlnIleLeuAspMetGlyGlyThrTrpGluArgAspThr 179
|||||
102 CAATTAGAGAGATTCTTGACATGGGTGGAGACGTGGATAGGGAGACG 151
|||||
180 ValValArgAlaLeuArgAlaAlaIYrAsnAsnProGluArgAlaIleAs 196
|||||
152 GTTGTTCGAGCCCTACGGCGAGCTTTTAACAATCTGACAGGGCTGTTC 201
|||||
196 pTYrLeuTYrSerGlyIleProGluAsnValGluAlaGlnProValAla 213
|||||
202 ATACTGTACTCTGTGATTCCTGAGGACAGAGAGTCCCTGTTGGAG 251
|||||
213 rGAlaProAlaAlaGlyGlnGlnThrAsnGlnAlaAlaSerProAla 229
|||||
252 GAAGTCCACCCAGCTGACAGGAGTAAATCAA.....CCGGCT 289
|||||
230 GlnProAlaValAlaLeuProValGlnProSerProAlaSerAla...G 245
|||||
290 CACCTCAACCTGCA.....GCACAACGACACCTGTCTCTGACGGCG 333
|||||
245 YProAsnAlaAsnProLeuAsnLeuPheProGlnGlyValProSerGly 262
|||||
334 ACCCAATGAGATCCCTGAATCTTCTCTCAAGGTCTCTCAGTGTGG 383
|||||
262 YSerAsnProGlyValValProGlyAlaGlySerGlyAlaLeuAspAla 278
|||||
384 GATCTAATACT.....GCTGTGTCGAACACCTTAGACTTT 418
|||||
279 LeuArgGlnLeuProGlnPheGlnAlaLeuLeuGlnLeuValGlnAla 295
|||||
419 CTAAAGAACAGTCAAGCTTCAAGCTTACGGGCAATGGTCAAGGCCAA 468
|||||
295 nProGlnIleLeuGlnProMetLeuGlnGluLeuGlyLYsGlnAsnPro 312
|||||
469 TCCACAATTTTGCAGCCCATGCTTCAAGAGTACGCAACAGATCCCC 518
|||||
312 InIleLeuArgLeuIleGlnGlnAsnGlnAlaGlnPheLeuArgLeuVal 328

```

```

519 ACCTAATGAGGCTTATACAGACACACGAGCTGATTTCTTCGCTTATC 568
|||||
329 AsnGlySerProGlnGlyGlyProGlnGlyAsnIleLeuGlnLeuAl 345
|||||
569 AATGAGCGCTTGTGAGAGAGAGAAAGCAACACGCTACTGGCCAGCTTC 618
|||||
345 aAlaAlaValProGlnThrLeuThrValThrProGlnGlnArgGlnAla 362
|||||
619 AGCAGCAATGCCACAGCTATATCTGTAAACCCGGAAGAGCGTGAAGCCA 668
|||||
362 LegIlnArgLeuGlnGlyMetGlyPheAsnArgGlnLeuValIleGlnVal 378
|||||
669 TAGAACCTCTTGAGACAGATGCGCTTGATCATACCTTGATCGAGGTT 718
|||||
379 PhePheAlaCysAsnLYsAspGlnLeuThrAlaAsnTYr 392
|||||
719 TTCTTTGCTTCGACACAAAT.GAAGAGCTCGCTGCTACTATAC 759
|||||

seq_name: gb_est2:BG445098

seq_documentation_block:
LOCUS      BG445098      899 bp      mRNA      linear      EST 15-MAR-2001
DEFINITION GA_Ea0026W08f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0026W08f, mRNA sequence.
ACCESSION  BG445098
VERSION    BG445098.1 GI:13354750
KEYWORDS   EST.
SOURCE     Gossypium arboreum.
ORGANISM   Gossypium arboreum.
REFERENCE  1 (bases 1 to 899)
AUTHORS   Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
          , D., Wood, T.C., Leslie, A. and Wilkins, T.A.
          An integrated analysis of the genetics, development, and evolution
          of the cotton fiber
          Unpublished (2000)
JOURNAL   Contact: Ming RA
          Clemson University Genomics Institute
          100 Jordan Hall, Clemson, SC 29634, USA
          Tel: 864 656 7288
          Fax: 864 656 4293
          Email: rwing@clemson.edu
          Seq primer: TAATACGACTCACTATAGG
          High quality sequence stop: 772.
          Location/Qualifiers
            source
              1..899
                /organism="Gossypium arboreum"
                /strain="AKA"
                /cultivar="8400"
                /db_xref="taxon:29729"
                /clone="GA_Ea0026W08f"
                /tissue_type="Fibers isolated from bolls harvested 7-10
                dpa"
                /lab_host="E. coli"
                /note="Vector: pBK-CMW; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT      256 a      206 c      215 g      221 t      1 others
ORIGIN

alignment_scores:
Quality:      817.50      Length:      319
Ratio:        3.296      Gaps:      9
Percent Similarity: 77.743      Percent Identity: 57.994

alignment_block:
US-09-805-550-2 x BG445098 ..

Align seg 1/1 to: BG445098 from: 1 to: 899

```

[illegible]

```

336 roglY 337
|||
891 AGGA 895

seq_name: gb_est1:AW399956

seq_documentation_block:
LOCUS   AW399956               623 bp    mRNA    linear    EST 07-FEB-2000
DEFINITION  707055C08.x1.707 - Mixed adult tissues from Walbot lab (SK) Zea
ACCESSION  mays cDNA, mRNA sequence.
VERSION    AW399956
KEYWORDS   AW399956.1  GI:6918426
SOURCE     EST.
ORGANISM   Zea mays.
            Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoidae; Andropogoneae; Zea.
            1 (bases 1 to 623)
            Walbot.V.
REFERENCE  Zea ESTs from various cDNA libraries sequenced at Stanford
AUTHORS   University
TITLE      Unpublished (1999)
JOURNAL    Contact: Walbot V
COMMENT    Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 707055 row: C column: 08.

FEATURES
            Location/Qualifiers
                1..623
                /organism="Zea mays"
                /cultivar="W23"
                /db_xref="taxon:4577"
                /clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"
                /tissue_type="tassel, kernel, silk, husk, root, leaf"
                /dev_stage="adult"
                /lab_host="DH10B"
                /note="Organ: tassel, kernel, silk, husk, root, leaf;
                Vector: pGAD10; Site.1: EcoRI; cDNA library from fully
                differentiated maize tissues from an active Mutator
                plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
                husk, root, leaf). Undirectionally cloned."
                husk, root, leaf). 122 t 1 others

BASE COUNT  158 a 175 c 167 g 122 t

ORIGIN
alignment_scores:
    Quality: 812.00      Length: 174
    Ratio: 4.749         Gaps: 0
    Percent Similarity: 98.276      Percent Identity: 95.977

alignment_block:
US-09-805-550-2 x AW399956  ..

Align seg 1/1 to: AW399956 from: 1 to: 623

1 MetUySleuAsnVallysThreUySGlyTrrAsnPhcGlUllGtUal 17
|||||
102 ATGAAGCTTAACGTCAAGACCCCTCAAGGGACCACTTGAGATCGAGGC 151
|||||
17 aserProAspAlaSerValAlaAspVallysaTgTlelGglUthrThg 34
|||||
152 GAGCCCCGATGCGTGGTCTGCTGACGTGAAGAGATCATTTGAGACACATC 201
|||||
34 lngUelnsrThrTyraGalaaspGlnglMetleUleTyrGlngly 50

```



```

|||||
202 AGGCTAGACTACTACCGGGGGGACGCAAAATGCTATATACCAAGG 251
51 Lys11leuLysAspGluThrThrLeuGluSerAsnGlyValAlaGluAs 67
252 AAAATCTCAAGGATGAGACCACTTGGAAAGCACGAGACTGCTGAGAA 301
67 nSerPheLeuVal11leuLeuSerLysAlaLysAlaSerSerSerGlyA 84
302 CACCTTCCTGTTATATATGTTGTCACAGGCTTAAGGCATCCTCGAGTG 351
84 laSerThrAlaThrThrAlaLysAlaProAlaThrLeuAlaGlnProAla 100
352 CTCTACCACTACTGCTGCAAAAGCTCTGCAACTGCGCCCAACCTGCT 401
101 AlProValAlaProAlaAlaSerValAlaArgThrProThrGlnAlaPr 117
402 GCCCTGTGCCCCCTGCTGCATCATGTTGCAAGAACCAACACACAGCTCC 451
117 oValAlaThrAlaGluThrAlaProProSerValGlnProGlnAlaAlaP 134
452 TGTGGCCACAGCTGAAGGACACCTCCAGTGCACCACTCAGGCTGCTC 501
134 roAlaAlaThrValAlaAlaAlaThrAspAspAlaAspValTyrSerGlnAla 150
502 CACCTGCTACGGTGTGCTACTGATGATGCTGATGTGTACAGACGACA 551
151 AlAserAsnLeuValPheGlyAsnAsnLeuGluGlnThrIleGlnGlnI 167
552 GCTTCAAACTTGTATCTGGCACAACAGCTTAGAACACTATCCAAACAAT 601
167 eLeuAspMetGlyGlyGlyThr 174
602 TCTTGACATGGGTGGTGTTACA 623

seq_name: gb_est2:BM078237

seq_documentation_block:
LOCUS BM078237 685 bp mRNA linear EST 14-NOV-2001
DEFINITION MEST116-H10.r3 ISUM4-TN Zea mays cDNA clone MEST116-H10 3', mRNA
sequence.
ACCESSION BM078237
VERSION BM078237.1 GI:16925169
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 685)
Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual bascall and confidence value were assigned using the
phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b
rt>). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/soflab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
CTA TAG)

```

```

BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
1..685
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST116-H10"
/clone_1ib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5',
AAGTGAAGAAATTCGGCGCCGACGAATTTTCTTTTCTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA polI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to COT value
of 5 based on the methods of Marcelo Bento Soares (genome
Research 6: 791-806, 1996)."
BASE COUNT 177 a 169 c 155 g 184 t
ORIGIN

alignment_scores:
Quality: 808.00 Length: 158
Ratio: 5.114 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.367

alignment_block:
US-09-805-550-2 x BM078237/rev ..

Align seg 1/1 to reverse of: BM078237 from: 1 to: 685

248 AlAsnProLeuAsnLeuPheProGlnGlyValProSerGlyGlySerAs 264
|||||
684 GCANAATCTTGAACCTTTTCTCAGGGGTCTCCAGAGTGAGGATCCAA 635
264 nProGlyValValProGlyAlaGlySerGlyAlaLeuAspAlaLeuArg 281
|||||
634 CCCAGGTGTTTCTCCAGTGCGAGATCGTGCCTTTCATCCCTTGGCAC 585
281 InLeuProGlnPheGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGln 297
|||||
584 AGCTTCCACAGTTTCAAGCACTCTTCAGTTAAGTCCAGGCTAATCCCAA 535
298 IleLeuGlnProMetLeuGlnGluLeuGlyLysGlnAsnProGlnIlele 314
|||||
534 ATCTTGACGCCAATGCTTCAAGACTAGTAAACAAACCCCAAAATCT 485
314 uArgLeuIleGlnGlnLysAsnGlnAlaGluPheLeuArgLeuValAsnGln 331
|||||
484 GCGGTGATTTCAGGAATAATCAAGCTGACTTCTCCCGCTGGTGAATGAT 435
331 eProGlnGlyGlyProGlyLysAsnIleLeuGlnGlnLeuAlaAlaAla 347
|||||
434 CTCTGAGGCTGTCCTGAGGAAACATACATGATGCACTGCGAGCTGCT 385
348 ValProGlnThrLeuThrValThrProGlnGluArgGluAlaIleGlnAr 364
|||||
384 GTGCCACAAACGCTGACAGTACCCCAAGAGAGAGGAGGCTATCCACAG 335
364 gLeuGlnGlyMetGlyPheAsnArgGluLeuValLeuGlnGluValPhePhe 381
|||||
334 GCTGAGGGAATGGGCTTCAACCGTGAAGCTTGTGCTGAATTTTCTTTG 285
381 lAcYAsnLysAspGluGluLeuThrAlaAsnTyrLeuLeuAspHisGly 397

```

```

|||||
284 CATGAAAGAGACGAGAGCTTACAGCCAACTACCTCTGATCATGGC 235
398 HsGlupheaspaspGlnGln 405
|||||
234 CATGAGTTTGACGACGACGACAA 211

seq_name: gb_est1:AM000280

seq_documentation_block:
LOCUS AM000280 565 bp mRNA linear EST 08-SEP-1999
DEFINITION 614010B04.y1 614 - root cDNA library from Walbot Lab zea mays cDNA,
mRNA sequence.
ACCESSION AM000280
VERSION AM000280.1 GI:5847201
KEYWORDS EST.
SOURCE zea mays.
ORGANISM zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614010 row: B column: 04.
FEATURES
SOURCE
1..565
location/Qualifiers
/organism="Zea mays"
/cultivar="W3"
/db_xref="taxon:4577"
/clone_id="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
/note="Organ: root; Vector: pBluescriptII SK+; Site_1:
ECORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"
BASE COUNT 139 a 133 c 148 g 145 t
ORIGIN
align_scores:
Quality: 803.00 Length: 157
Ratio: 5.115 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.726

alignment_block:
US-09-805-550-2 x AM000280 ..

Align seg 1/1 to: AM000280 from: 1 to: 565
249 AsnProLeuAsnLeuPheProGlnGlyAlaProSerGlyGlySerAsnPr 265
|||||
1 AATCTTTGAAACCTTTTCTCAGGGGTGTTCCAAAGTGGGTCCAAACCC 50
265 cblYValValProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnL 282
|||||
51 AGGCGTATATCCAGGTCGCGATCGTCCCTTGATGCTTGCCGACAC 100
282 euProGlnPheGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGlnInle 298
|||||
101 TTCCACAGATTCAAGCAGCTCTTCAATTAGTCCAGGCTAATCTCAATC 150
299 LeuGlnProMetLeuGlnGlnLeuGlnLysGlnAsnProGlnInleLeuAr 315

```

```

|||||
151 TTGACGCCAATGCTTCAAGAGCTAGGTAACAACCAACCAAAATTCCTGGC 200
315 gleuIleGlnGluAsnGlnAlaGluPheLeuArgLeuValAsnGluSep 332
|||||
201 GTTGATTCAGGAAATCAAGCTGAGTTTCTCCGCTTGGAATGAAATC 250
332 roGluGlyGlyProGlyGlyAsnIleLeuGlnLeuAlaAlaVal 348
|||||
251 CTGAGGGTGCTCTGGAGGGAACATCTAGTCACTGACAGCTGCTGTG 300
349 ProGlnThrLeuThrValThrProGluGluArgGluAlaIleGlnArg 365
|||||
301 CCACAAACGCTGACAGTACCCAGAGGAACGAGGACTATCCAGCGCT 350
365 uGluGlyMetGlyPheAsnArgGluLeuValLeuGlnValAlaPheAlaC 382
|||||
351 CAGGGAATGGGGTTCAACCGTGAGCTTGCTAGAGATTCTTTGCAT 400
382 yaAsnLysAspGluGluLeuThrAlaAsnTyrLeuLeuAspHisGlyHis 398
|||||
401 GCAACAAGAGCAAGAGCTTACAGCCAACTACTCTGTGATGATGCGCAT 450
399 GluPheAspAspGlnGln 405
|||||
451 GAGTTTGACGACGACGACCA 471

seq_name: gb_est2:BG445328

seq_documentation_block:
LOCUS BG445328 810 bp mRNA linear EST 15-MAR-2001
DEFINITION GA_Ea0027L22f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0027L22f, mRNA sequence.
ACCESSION BG445328
VERSION BG445328.1 GI:1354980
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE
AUTHORS Wing,R.A., Fritsch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
'D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGCG
High quality sequence stop: 767.
FEATURES
SOURCE
1..810
location/Qualifiers
/organism="Gossypium arboreum"
/strain="AKA"
/db_xref="taxon:29729"
/clone_id="GA_Ea0027L22f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/note="Vector: pBR-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 212 a 204 c 198 g 193 t
ORIGIN
align_scores:

```

Quality: 781.50 Length: 269
 Ratio: 3.618 Gaps: 8
 Percent Similarity: 80.297 Percent Identity: 63.197

alignment block:
 US-09-805-550-2 x BG445328 ..

Align seg 1/1 to: BG445328 from: 1 to: 810

```

82 SerGlyAlaSerThrAlaThrAlaValAlaProAlaThrLeuAlaI 98
   ||| ||||| ||||| ||| ||||| |||
7 TCACAGCTTCAACAGCTCTACAAAGAAAGCTCTGAGGACGTAATCT 56
   ||| ||||| ||||| ||||| ||||| |||||
98 nProAlaAlaProValAlaProAlaAlaSerValAlaArgThrProThrg 115
   ||||| ||||| ||||| ||||| ||||| |||||
57 GCACAGAGCTGCA...GCACAGCTTCTACT..... 84
   ||||| ||||| ||||| ||||| ||||| |||||
115 lAlaAlaProValAlaAlaThrAlaAlaThrProSerValAlaProGln 131
   ||||| ||||| ||||| ||||| ||||| |||||
85 ..GCACCTTTCACAGCTCAGTATGCT....GCAGTGCCTACTGAA 126
   ||||| ||||| ||||| ||||| ||||| |||||
132 AlAlaAlaProAlaAlaThrValAlaAlaThrAspAlaAlaPylTyrSe 148
   ||||| ||||| ||||| ||||| ||||| |||||
127 TCAGCTCCTGCTTCTCAGTACTCTTCTGATTCATGATCTTATGG 176
   ||||| ||||| ||||| ||||| ||||| |||||
148 rGlnAlaAlaSerAsnLeuValPheGlyAsnAsnLeuGlnThrIleg 165
   ||||| ||||| ||||| ||||| ||||| |||||
177 CCAGAGAGCATCTACCTGCTGAGGAGTAATTAGAGCAATCC 226
   ||||| ||||| ||||| ||||| ||||| |||||
165 lGlnIleLeuAspMetGlyGlyGlyThrTrpGluArgAspThrValAla 181
   ||||| ||||| ||||| ||||| ||||| |||||
227 AACAGATTCTTGATATGGTGGAGGACCTGGGACAGGACCTGTTGTC 276
   ||||| ||||| ||||| ||||| ||||| |||||
182 ArgAlaLeuArgAlaAlaTyrAsnAsnProGluArgAlaIleAspTyrLe 198
   ||||| ||||| ||||| ||||| ||||| |||||
277 CAGGCCCTTGCTGCTGTTATATAACCCAGAGAGCTGTGAATTTT 326
   ||||| ||||| ||||| ||||| ||||| |||||
198 uTyrSerGlyIleProGluAsnValGluAlaGlnProValAlaArgAlaP 215
   ||||| ||||| ||||| ||||| ||||| |||||
327 GTATTTGGGATCCCGAGCAAGCTGMAAGCTCCACCTGGCCGCTGCTC 376
   ||||| ||||| ||||| ||||| ||||| |||||
215 rAlaAlaAlaGlyGlnIleThrAsnGlnIleThrAlaSerProAlaGlnPro 231
   ||||| ||||| ||||| ||||| ||||| |||||
377 CTGTAGTGGGCAACCAAC...TCTGCTGCAACCTCAACAGCT 423
   ||||| ||||| ||||| ||||| ||||| |||||
232 AlAlaValAlaLeuProValGlnProSerProAlaSerAlaGlyProAsnAl 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
424 GCACAAAGCGCAGCTATT.....CTGCAAGT...GGACCAATGC 461
   ||||| ||||| ||||| ||||| ||||| |||||
248 aAsnProLeuAsnLeuPheProGlnGlyValProSerGlyIleSerAsnP 265
   ||||| ||||| ||||| ||||| ||||| |||||
462 AAATCCATTCAGACCTCTTCCCAAGGCGCTCCCAACATCGGTGCAAGT. 510
   ||||| ||||| ||||| ||||| ||||| |||||
265 rGlyValValProGlyAlaGlySerGlyAlaLeuAlaSerAlaLeuArgGln 281
   ||||| ||||| ||||| ||||| ||||| |||||
511 .....GGTGTGGGGGCTGCACTCTGTGATTTTTCAGGAAC 546
   ||||| ||||| ||||| ||||| ||||| |||||
282 LeuProGlnPheGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGlnIle 298
   ||||| ||||| ||||| ||||| ||||| |||||
547 AGTCACAGCTTTCAGCTTGGCGAAGATGGTGAAGCCCAATCCACAAT 596
   ||||| ||||| ||||| ||||| ||||| |||||
298 eLeuGlnProMetLeuGlnGlnLeuGlyIleGlnAsnProGlnIleLeuAl 315
   ||||| ||||| ||||| ||||| ||||| |||||
597 ATTCGAGCCATTCCTTCACAGAGTGGGAAACAAATCCAAATTAATGA 646
   ||||| ||||| ||||| ||||| ||||| |||||
315 rGlyLeuIleGlnIleGlnAlaGlnPheLeuArgLeuValaGlnIleUser 331
   ||||| ||||| ||||| ||||| ||||| |||||
647 GACTTATTCAGAGCATCAGGAGTACTTCTGCTTGAATCAATGAAGACT 696
   ||||| ||||| ||||| ||||| ||||| |||||
332 ProGlnGlyIleProGlyIleAsnIleLeuGlyGlnIleAlaAlaAlaAla 348
   ||||| ||||| ||||| ||||| ||||| |||||
697 GCGAAGAGTGAGAG...GGAACATTNTGGGCAATTACTCTAGGAGAT 743
   ||||| ||||| ||||| ||||| ||||| |||||

```

348 lProGln 350
 :|||||
 744 GCCACAG 750

seq_name: gp_est2:BG365760

seq_documentation_block:

LOCUS BG365760 906 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSM10004B16f Hordeum vulgare 20 DAP spike EST library HVCDA0010
 (20 DAP) Hordeum vulgare cDNA clone HVSM10004B16f, mRNA sequence.
 ACCESSION BG365760
 VERSION BG365760.2 GI:16323859
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae
 ; Triticeae; Hordeum.
 1 (bases 1 to 906)
 Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
 ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Chol,D.W., Fenton
 ,R.D., Close,S.J., Oates,R. and Main,D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex 20 DAP spike cDNA library
 Unpublished (2001)
 On Mar 8, 2001 this sequence version replaced gi:13254859.
 Contact: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Total bp bases = 406
 Seq primer: AATTAACTCCTCAAGAGG
 High quality sequence stop: 657.
 Location/Qualifiers

FEATURES

source

1..906
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSM10004B16f"
 /clone_lib="Hordeum vulgare 20 DAP spike EST library
 HVCDA0010 (20 DAP)"
 /issue_type="20 DAP spike"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP. Site_1: EcoRI. Site_2: XhoI.
 Plants were grown in the greenhouse at the University of
 California, Riverside (Fenton, SJ Close, TJ Close). Whole
 spikes with awns trimmed were collected at 20 DAP (Fenton
). Total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, and 1 million
 pfu were in vivo excised to give plasmid SK(-) cDNA
 phagemids in the TJ Close lab at the University of
 California, Riverside (Choi). Phagemids were plated and
 picked at the Clemson University Genomics Institute (CUGI)
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 , Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/gsgpages/bgn/31/cover.html)"
 BASE COUNT 206 a 241 c 246 g 212 t 1 others

alignment_scores: Length: 287
 Quality: 781.50 Gaps: 10
 Ratio: 3.383
 Percent Similarity: 80.488 Percent Identity: 65.505

alignment_block:
 US-09-805-550-2 x BG365760 ..

Align seg 1/1 to: BG365760 from: 1 to: 906

```

1  MetLysLeuAsnValIleuThrLeuLysGlyThrAsnProGlnIleGluAl 17
   |||||||.....|.....|.....|.....|.....|.....|.....|
67  ATGAAGCTCAACGTAAAGACCTCAAGGACACACCTCGAGATGAGAGC 116
   |||||||.....|.....|.....|.....|.....|.....|.....|
17  ASerProAspAlaSerValAlaAspValLysArgIleIleGluThrThrG 34
   |||||||.....|.....|.....|.....|.....|.....|.....|
117  GACCCCGAGTCCTCGTGGGTGAGCAAGAGACTCATCGAGAGTGTCTC 166
   |||||||.....|.....|.....|.....|.....|.....|.....|
34  lnglyGlnSerThrTyrArgAlaAspGlnIleMetLeuIleTyrGlnGly 50
   |||||||.....|.....|.....|.....|.....|.....|.....|
167  AGGGGCAAAATGTGTACCTCGCATCAGCTGATCATATATATCAAGCA 216
   |||||||.....|.....|.....|.....|.....|.....|.....|
51  LysIleLeuLysAspGluThrThrLeuGlnSerAsnGlyValAlaGluAs 67
   |||||||.....|.....|.....|.....|.....|.....|.....|
217  AAAATCTGAAAGATGATACCACTGTGATGCTATCAAGGTTGCAAGAA 266
   |||||||.....|.....|.....|.....|.....|.....|.....|
67  nSerPheLeuValIleMetLeuSerLysAlaLysAlaSerSerSerGlyA 84
   |||||||.....|.....|.....|.....|.....|.....|.....|
267  CAGTTCCTGTTATATGCTGTCTAAGCCCTAAGCCGTCATCTAGTGGCG 316
   |||||||.....|.....|.....|.....|.....|.....|.....|
84  lAserThrAlaThrThrAlaLysAlaProAlaThrLeuAlaGlnProAla 100
   |||||||.....|.....|.....|.....|.....|.....|.....|
317  CTCTCTTCGCT.....TCAAAGCACCTGTATGTCAGTCTCAACCTGCT 360
   |||||||.....|.....|.....|.....|.....|.....|.....|
101  AlaProValAla.....ProAlaAlaSerValAlaAla 111
   |||||||.....|.....|.....|.....|.....|.....|.....|
361  ACCCAGAGTGTGCTGCTACTACCTGCTGCTGCTGCTGCTGCTGCTGCA 410
   |||||||.....|.....|.....|.....|.....|.....|.....|
111  gThr...ProThrGlnAlaProValAlaThrAlaGlnThrAlaProProS 127
   |||||||.....|.....|.....|.....|.....|.....|.....|
411  ATCAACACCTTCGCAAGCACCTGTGCTGATCTGATCAACGCGCTCCCA 460
   |||||||.....|.....|.....|.....|.....|.....|.....|
127  erValGlnProGlnAla.....AlaProAlaAlaThrValAlaAla 140
   |||||||.....|.....|.....|.....|.....|.....|.....|
461  GTGCACACACTTCACGCTGTCTGATCTCCAGCTGCTGCTGCTGCTGCA 510
   |||||||.....|.....|.....|.....|.....|.....|.....|
141  ThrAspAspAlaAspValLysSerGlnAlaAlaSerAsnLeuValIle 157
   |||||||.....|.....|.....|.....|.....|.....|.....|
511  TCAGCGCATGCTGATCTATACGCTGAGCTGATCAAACTTGTCTCTCG 560
   |||||||.....|.....|.....|.....|.....|.....|.....|
157  yAsnAsnLeuGlnGlnThrIleGlnGlnIleLeuAspMetGlyGlyT 174
   |||||||.....|.....|.....|.....|.....|.....|.....|
561  CGGCATCTAGAACAGACAGTCCATCAATCTTGACATGGGTGCTGCA 610
   |||||||.....|.....|.....|.....|.....|.....|.....|
174  hTrpGlnArgAspThrValAlaArgAlaLeuArgAlaAlaLysTrpAsn 190
   |||||||.....|.....|.....|.....|.....|.....|.....|
611  CCGTGAAGCTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 660
   |||||||.....|.....|.....|.....|.....|.....|.....|
191  ProGlnArgAlaAlaAspTyrLeuTyrSerGlyIleProGlnLysValG 207
   |||||||.....|.....|.....|.....|.....|.....|.....|
661  CCGTGAAGGCTATGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
   |||||||.....|.....|.....|.....|.....|.....|.....|
207  uAlaGlnProValAlaArgAlaProAlaAlaGly..GlnGlnThrAsnG 223
   |||||||.....|.....|.....|.....|.....|.....|.....|
711  GGCCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
   |||||||.....|.....|.....|.....|.....|.....|.....|
223  nGlnAlaAlaSerProAlaGlnProAlaValAlaLeu..ProValGlnPro 239
   |||||||.....|.....|.....|.....|.....|.....|.....|
761  TCAGGCTCAATCTAAGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 810
   |||||||.....|.....|.....|.....|.....|.....|.....|
240  Ser...ProAlaSerAlaGlyPro..AsnAlaAsnProLeuAsnLeuPhe 255
   |||||||.....|.....|.....|.....|.....|.....|.....|
811  TCTGTGTGGGTCTCTGTGTGGGTCTTAAGCAAAATCTTTAAACCTTTT 860
   |||||||.....|.....|.....|.....|.....|.....|.....|

```

255 roGlnGlyVal..ProSerGlyLysSerAsnProGlyValProGlyAl 271
 |||||||.....|.....|.....|.....|.....|.....|.....|
 861 CACAGGCTGTTCGCGGTGGGTGGGCC.....ATTCCTGGGCC 898

271 agly 272
 |||||
 899 CGGA 902

seq_name: gb_estl:AV928200

seq_documentation_block:

LOCUS AV928200 750 bp mRNA linear EST 18-JAN-2002
 DEFINITION AV928200 K. Sato unpublished cDNA library, cv. Haruna Nijo second
 leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA
 clone basd27f18 3', mRNA sequence.
 AV928200
 AV928200.1 GI:18223997

KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare.
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 750)

REFERENCE Sato, K., Saitoh, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 Unpublished (2002)
 COMMENT Contact: Tadasu Shin-1
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

FEATURES
 location/Qualifiers

1..750
 /organism="Hordeum vulgare subsp. vulgare"
 /cultivar="Haruna Nijo"
 /db_xref="taxon:112509"
 /clone="basd27f18"
 /clone_1lb="K. Sato unpublished cDNA library, cv. Haruna
 Nijo second leaf stage seedling leaves"
 /issue_type="seedling leaves"
 /dev_stage="second leaf stage"
 BASE COUNT 190 a 194 c 181 g 183 t 2 others
 ORIGIN

alignment_scores:
 Quality: 774.00 Length: 194
 Ratio: 4.423 Gaps: 2
 Percent Similarity: 90.206 Percent Identity: 81.443

alignment_block:
 US-09-805-550-2 x AV928200/rev ..

Align seg 1/1 to reverse of: AV928200 from: 1 to: 750

```

213  ArgAlaProAlaAlaGlyGlnGlnThr...AsnGlnAlaAlaSerPr 228
   |||||||.....|.....|.....|.....|.....|.....|
750  CGAGCACCTGCTGCTGCTCAACAGCACAAACCTGCAAGCTCATCCCA 701
   |||||||.....|.....|.....|.....|.....|.....|
228  oAlaGlnProAlaValAlaLeuProValGlnProSer...ProAlaSer 244
   |||||||.....|.....|.....|.....|.....|.....|
700  GGCTCAGGCTGACACTCTACCGCGAGTGCAGCACTGTGTGTCTCTG 651
   |||||||.....|.....|.....|.....|.....|.....|
244  lAglyProAsnAlaAsnProLeuAsnLeuPheProGlnGlyValProSer 260
   |||||||.....|.....|.....|.....|.....|.....|
650  CTGGGCTCAATGCGAATCCTTAACCTTTCCACAGGCTGCTCCAACT 601
   |||||||.....|.....|.....|.....|.....|.....|
261  GlyGlySerAsnProGlyValValProGlyAlaGlySerGlyAlaLeuAs 277
   |||||||.....|.....|.....|.....|.....|.....|

```

```

600 GTGGGGCCAATGCTGCTGCTGGTGCGTGCCGGTGCCGGTGCCTTGA 551
277 pAlaLeuArgGlnLeuProGlnPheGlnAlaLeuLeuGlnLeuValGlnA 294
|||||
550 TGCATTGCGAGAGTTCCACAGCTGCTTGCATTGGTCCAGG 501
|||||
294 LaAsnProGlnIleLeuGlnProMetLeuGlnIleuGlyLysGlnAsn 310
|||||
500 CTAATCCCCCAATCTCAGCCCAATGCTCAAGAGCTGGGGAAACAAT 451
|||||
311 ProGlnIleLeuArgLeuIleGlnGluAsnGlnAlaGluPheLeuArgLe 327
|||||
450 CCAAGATCCTGCGGTGATTCAGGAAATCAGGCTGATTTCTCCGCT 401
|||||
327 uValAsnGluSerProGlnGlyGlyProGlnGlyAsnIleLeuGlyGlnL 344
|||||
400 GGTAAATGAACAACCTGAGAGTGCTGGCGGAATATACTAGCGCAC 351
|||||
344 euAlaIaIaValProGlnThrLeuThrValThrProGlnGluArgGlu 360
|||||
350 TGGCAGCTCAAAATGCCACAGGCACTCAAGTTACTCCAGAAAGCGGAG 301
|||||
361 AlaIleGlnArgLeuGlnGlyMetGlyPheAsnArgGluLeuValLeuG 377
|||||
300 GCCATCCAGCGGCTTGAGTCAATGGGTTCAATGCTGAGCTTGTTGA 251
|||||
377 uValPhePheAlaCysAsnLysAspGlnIleuLeuThrAlaAsnTyrLeuL 394
|||||
250 GGTCTTCTTGCATGCAACAGGATGAAGAACTGGCTGCCAATATCTTT 201
|||||
394 euAspHisGlyHisGluPheAspAspGlnGln 404
|||||
200 TGGATCATGGCCACGAGTTTGAGGACACACAA 169

```

